



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 147441

TO: Amy H Bowman
Location: REM/2C18
Art Unit: 1635
Tuesday, March 22, 2005

Case Serial Number: 10/646391

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Bowman,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

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STIC-Biotech/ChemLib

147441

From: Bowman, Amy
Sent: Thursday, March 10, 2005 3:29 PM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-10/646,391 (2)

Hello,
I need SEQ ID NO:4 searched from application number 10/646,391.
Thank you,
Amy Bowman
AU 1635

RECEIVED
MAR 10 2005
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STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 07:42:25 ; Search time 1430 Seconds
(without alignments)
711.580 Million cell updates/sec

Title: US-10-646-391A-4
Perfect score: 21
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	21	100.0	255	6	CQ693037	CQ693037 Sequence
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7	21	100.0	275	6	AX895152	AX895152 Sequence
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9	21	100.0	306	6	CQ684015	CQ684015 Sequence
10	21	100.0	396	6	AR391192	AR391192 Sequence
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VERSION						
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ORGANISM	Homo sapiens					
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AUTHORS		Treatment of melanoma by reduction in clusterin levels				
TITLE		Patent: WO 2004018675-A 4 04-MAR-2004;				
JOURNAL		The University of British Columbia (CA); Gleave, Martin E. (CA)				
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ACCESSION	CQ786178					
VERSION	CQ786178.1	GI:45721281				
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ORGANISM	Homo sapiens					
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AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
JOURNAL      Gonos,E.
FEATURES     Rnai probes targeting cancer-related proteins
              Patent: WO 2004018676-A 66 04-MAR-2004;
              The University of British Columbia (CA)
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ACCESSION  AR302789
VERSION     AR302789.1 GI:31691276
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 181)
AUTHORS    Kirschling,D.J., Gudkov,A. and Roninson,I.B.
TITLE      Genes and genetic elements associated with sensitivity to
            platinum-based drugs
JOURNAL    Patent: US 6541603-A 19 01-APR-2003;
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DEFINITION Sequence 14 from patent US 6541603.
ACCESSION  AR302784
VERSION     AR302784.1 GI:31691271
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 195)
AUTHORS    Kirschling,D.J., Gudkov,A. and Roninson,I.B.
TITLE      Genes and genetic elements associated with sensitivity to
            platinum-based drugs
JOURNAL    Patent: US 6541603-A 14 01-APR-2003;
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REFERENCE  1
AUTHORS    Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE      Compositions and methods relating to osteoarthritis
JOURNAL    Patent: WO 02070737-A 37963 12-SEP-2002;
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ACCESSION  CQ688092
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KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
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REFERENCE  1
AUTHORS    Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE      Compositions and methods relating to osteoarthritis
JOURNAL    Patent: WO 02070737-A 33018 12-SEP-2002;
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VERSION AX895152.1 GI:40050036
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 11015 06-SEP-2000;
Genset (FR)
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DEFINITION Sequence tag and encoded human protein.
ACCESSION BD030685
VERSION BD030685.1 GI:22572427
KEYWORDS JP 2001269182-A/6931.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 275)
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 6931 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/6931
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
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ACCESSION CQ684015
VERSION CQ684015.1 GI:42207944
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 28941 12-SEP-2002;
Chondrogene Inc. (CA)
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ACCESSION AR391192
VERSION AR391192.1 GI:40114652
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 396)
AUTHORS Xu, J. and Stolk, J.A.
TITLE Ovarian tumor sequences and methods of use therefor
JOURNAL Patent: US 6613515-A 15 02-SEP-2003;
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ACCESSION AR392897
VERSION AR392897.1 GI:40118137
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 396)
AUTHORS Xu,J. and Stolk,J.A.
TITLE Compositions and methods for the therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 6617109-A 15 09-SEP-2003;
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DEFINITION Sequence 15 from patent US 6710170.
ACCESSION AR489627
VERSION AR489627.1 GI:47256674
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 396)
AUTHORS Xu,J., Stolk,J.A., Algate,P.A. and Fling,S.P.
TITLE Compositions and methods for the therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 6710170-A 15 23-MAR-2004;
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VERSION AR493868.1 GI:47266388
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 396)
AUTHORS Stolk,J.A., Molesh,D.A., Fling,S.P. and Xu,J.
TITLE Compositions and methods for the therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 6720146-A 15 13-APR-2004;
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ACCESSION AX093197
VERSION AX093197.1 GI:13509646
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xu,J. and Stolk,J.A.
TITLE Ovarian tumor sequences and methods of use therefor
JOURNAL Patent: WO 0118046-A 15 15-MAR-2001;
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ACCESSION AR421770
VERSION AR421770.1 GI:40176880
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 482)
AUTHORS Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
TITLE EST's and encoded human proteins
JOURNAL Patent: US 6639063-A 13267 28-OCT-2003;
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Job time : 1433 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 04:56:41 ; Search time 235 Seconds
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Title: US-10-646-391A-4
Perfect score: 21
Sequence: 1 cagcagcagagtcttcatcat 21

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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13	21	100.0	396	12	ADM43275 Human ova
14	21	100.0	461	9	ACH44960 Human foe
15	21	100.0	462	9	ACH15312 Human adu
16	21	100.0	465	9	ACH44965 Human foe
17	21	100.0	490	9	ACH25299 Human adu
18	21	100.0	491	3	AAC03751 Human sec
19	21	100.0	491	9	ACH30243 Human tes
20	21	100.0	492	9	ACH43944 Human tes

C 21	21	100.0	512	2	AAV89150	Aav89150 EST clone
C 22	21	100.0	572	2	AAZ42136	Aaz42136 Human nor
C 23	21	100.0	704	6	ABQ56105	Abq56105 Human ova
C 24	21	100.0	922	3	AAA43857	Aaa43857 Human sec
C 25	21	100.0	1024	10	ABZ83527	Abz83527 Toxicolog
C 26	21	100.0	1067	8	ACC90611	Acc90611 Human CGD
C 27	21	100.0	1117	8	ACC90613	Acc90613 Human CGD
C 28	21	100.0	1315	8	ACC90621	Acc90621 Human CGD
C 29	21	100.0	1369	8	ACC90610	Acc90610 Human CGD
C 30	21	100.0	1373	8	ACC90622	Acc90622 Human CGD
C 31	21	100.0	1451	10	ADI02673	Adi02673 Human cDN
C 32	21	100.0	1568	5	AAS44948	Aas44948 cDNA enco
C 33	21	100.0	1589	6	ABS78654	Abs78654 Human cDN
C 34	21	100.0	1610	8	ACC90609	Acc90609 Human CGD
C 35	21	100.0	1648	6	ABN99656	Abn99656 Human clu
C 36	21	100.0	1651	2	AAQ11503	Aaq11503 Cytolysis
C 37	21	100.0	1651	6	ABN99666	Abn99666 Human clu
C 38	21	100.0	1651	12	ADP13327	Adp13327 Renal cel
C 39	21	100.0	1676	8	ACA64877	Aca64877 Human clu
C 40	21	100.0	1676	10	ADE85040	Ade85040 Farnesyl
C 41	21	100.0	1676	11	ADN95595	Adn95595 Human BEC
C 42	21	100.0	1676	12	ADL70403	Adl70403 Human clu
C 43	21	100.0	1676	12	ADN05798	Adn05798 Antipsori
C 44	21	100.0	1676	13	ACN38778	Acn38778 Tumour-as
C 45	21	100.0	1678	4	AAH23086	Aah23086 Osteoarth

ALIGNMENTS

RESULT 1
AAA94226
ID AAA94226 standard; DNA; 21 BP.

XX AAA94226;

XX 12-JAN-2001 (first entry)

DE Human testosterone-repressed prostate message-2 antisense oligo #2.

XX Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.

OS Homo sapiens.

PN WO200049937-A2.

XX 31-AUG-2000.

PF 25-FEB-2000; 2000WO-US004875.

XX 26-FEB-1999; 99US-0121726P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Gleave M, Rennie PS, Miyake H, Nelson C;

XX WPI; 2000-533132/48.

XX Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene.

XX Claim 3; Page 36; 38pp; English.

XX The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed at human
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC gene. These include prostate cancer, renal cell cancer and some breast
CC cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective

XX SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 2
ACF36398
ID ACF36398 standard; DNA; 21 BP.
XX
AC ACF36398;
XX
DT 18-DEC-2003 (first entry)
XX
DE TRPM-2 antisense oligonucleotide.
XX
KW TRPM-2; testosterone-repressed prostate message-2; cytotstatic; androgen;
KW prostate cancer; anti-apoptotic protein; antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003072591-A1.
XX
PD 04-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US005305.
XX
PR 22-FEB-2002; 2002US-00080794.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;
XX
DR WPI; 2003-689981/65.
XX
PT New modified antisense oligonucleotide, useful particularly for treating
PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.
XX
PS Claim 1; Page 25; 44pp; English.
XX
CC The invention relates to a compound consisting of an oligonucleotide with
CC a phosphorothioate backbone throughout, in which: (a) sugars on
CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the
CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at
CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence
CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive
CC prostatic cancer cells to the androgen-independent state, in vivo or in
CC vitro; (b) to treat prostatic cancer (after initially withdrawing
CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer
CC cells (prostatic, renal, non-small cell lung, urothelial transitional,
CC ovarian and some breast cancer cells) that express abnormal levels of
CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)
CC increase stability in vivo and activity (both in vivo or in vitro) and
CC result in a synergistic increase in effect when (I) is used with
CC chemotherapeutic agents or other antisense oligonucleotides directed
CC against other antiapoptotic genes. The present sequence represents a
CC specific example of an anti-apoptotic protein TRPM-2 (testosterone-
CC repressed prostate message-2) antisense oligonucleotide
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21

Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 3
ADM83069
ID ADM83069 standard; DNA; 21 BP.
XX
AC ADM83069;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human TRPM-2 antisense oligonucleotide #4.
XX
KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;
KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;
KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..21
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
PN US2003158130-A1.
XX
PD 21-AUG-2003.
XX
PF 28-SEP-2001; 2001US-00967726.
XX
PR 25-FEB-2000; 2000WO-US004875.
PR 28-SEP-2000; 2000US-0236301P.
PR 10-AUG-2001; 2001US-00913325.
XX
PA (GLEA/) GLEAVE M.
PA (RENN/) RENNIE P S.
PA (MIYA/) MIYAKE H.
PA (NELS/) NELSON C.
PA (ZELL/) ZELLWEGER T.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;
XX
DR WPI; 2003-778017/73.
XX
PT Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells
PT that expresses testosterone-repressed prostate message-2 (TRPM-2)
PT comprises administering a composition that inhibits expression of TRPM-2.
XX
PS Claim 4; SEQ ID NO 4; 14pp; English.
XX
CC The present invention provides a method for treating cancer in which
CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).
CC The invention is useful for enhancing the chemo-sensitivity or radiation-
CC sensitivity of cancer cells for treating cancer such as prostate cancer,
CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma
CC (RCC). The invention is also useful in antisense gene therapy. The
CC present sequence is human testosterone-repressed prostate message-2 (TRPM
CC -2) antisense oligodeoxyribonucleotide (ODN).
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 4
ADL70406
ID ADL70406 standard; DNA; 21 BP.
XX
AC ADL70406;
XX
DT 20-MAY-2004 (first entry)
XX
DE Antisense oligonucleotide to human clusterin.
XX
KW Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..21
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate nucleotides"
FT modified_base 1..4
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'O-methoxyethyl modifications"
FT modified_base 18..21
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'O-methoxyethyl modifications"
XX
PN WO2004018675-A1.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-CA001276.
XX
PR 21-AUG-2002; 2002US-0405193P.
PR 03-SEP-2002; 2002US-0408152P.
PR 02-DEC-2002; 2002US-0319748P.
PR 20-MAY-2003; 2003US-0472387P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (GLEA/) GLEAVE M E.
PI Jansen B;
XX
DR WPI; 2004-226851/21.
XX
PT Treating melanoma in a mammalian subject comprises administering to the
PT subject a therapeutic agent effective to reduce the effective amount of
PT clusterin in the melanoma cells.
XX
PS Claim 7; SEQ ID NO 4; 32pp; English.
XX
CC The present sequence is that of an antisense oligonucleotide targeted to
CC human clusterin ADL70403. The invention relates to the treatment of
CC melanoma through reduction in the effective amount of clusterin. The
CC therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421
CC or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.
CC The antisense oligonucleotides are complementary to a region of the
CC clusterin mRNA spanning either the translation initiation site or the
CC termination site. They may be modified to increase stability in vivo,
CC e.g. they may be employed as phosphorothioate derivatives and may have 2'
CC -O-(2-methoxyethyl) (MOE) modifications in the 5' and 3' 'wings'. The
CC present antisense oligonucleotide is particularly preferred. It is
CC targeted to the translation initiation codon and next 6 codons of the
CC human clusterin sequence. It has a phosphorothioate backbone throughout
CC and MOE wings, the remaining nucleotides being 2'-deoxynucleotides. In an
CC example from the invention, this antisense oligonucleotide provided a
CC dose-dependent down-regulation of clusterin in human melanoma cells,
CC leading to an increase in apoptotic cell death. In one melanoma cell line
CC (607B) this alone was sufficient to lead to complete cell death. In
CC another melanoma cell line, the surviving cells showed increased

CC sensitivity to subsequent treatment with cisplatin. A claimed method for
CC regulating expression of bcl-xL in a subject or cell line comprises
CC administering an agent effective to modulate the amount of clusterin
CC expression. In clusterin-expressing cells, expression of bcl-xL is down-
CC regulated when the effective amount of clusterin is reduced. Such
CC inhibition is significant because bcl-xL is known to act as an inhibitor
CC of apoptosis.
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 5
ADL70521/c
ID ADL70521 standard; cDNA; 23 BP.
XX
AC ADL70521;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human clusterin target for RNAi.
XX
KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004018676-A2.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-CA001277.
XX
PR 21-AUG-2002; 2002US-0405193P.
PR 03-SEP-2002; 2002US-0408152P.
PR 20-MAY-2003; 2003US-0472387P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
XX
DR WPI; 2004-226852/21.
XX
PT New RNA molecule less than 49 bases and having a sequence effective to
PT mediate degradation or block translation of mRNA that is the
PT transcriptional product of a target gene, useful for treating Alzheimer's
PT disease or cancer.
XX
PS Example 6; SEQ ID NO 66; 63pp; English.
XX
CC The present sequence is a human clusterin cDNA target for a double-
CC stranded short interfering RNA (siRNA) of the invention ADL70522-
CC ADL70523. It was used in an example from the invention to demonstrate
CC clusterin gene silencing in PC-3 prostate cancer cells. Clusterin, also
CC known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC tumour cells following androgen withdrawal, and has also been shown to be
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC siRNAs of the invention can be used alone or in combination with other
CC chemotherapy or apoptosis inducing treatments for the treatment of
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC anaplastic large cell lymphoma and melanoma, and also for the treatment

CC of Alzheimer's disease.
XX Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 21; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
|||||
Db 23 CAGCAGCAGAGTCTTCATCAT 3

RESULT 6
AAT00416/c
ID AAT00416 standard; cDNA; 195 BP.
XX
AC AAT00416;
Xx 26-MAR-1996 (first entry)
Dt Genetic suppressor element HL7.1.
XX
DE Genetic suppressor element; GSE; platinum-based drug; cisplatin;
XX chemotherapy; HL7.1; testosterone-repressed prostatic message-2; TRPM-2;
KW ss.
KW Synthetic.
XX OS
XX WO9522612-A2.
PN 24-AUG-1995.
PD 22-FEB-1995; 95WO-US002303.
XX 22-FEB-1994; 94US-00199900.
PR (UNII) UNIV ILLINOIS FOUND.
XX
PI Kirschling DJ, Gudkov A, Roninson IB;
XX WPI; 1995-302718/39.
DR
XX Genetic suppressor elements which confer resistance to platinum-based
XX drugs, eg. cisplatin, on cancer cells - useful for enhancement of
PT chemotherapy, and for diagnosis of resistance to these drugs.
PT
XX Claim 14; Fig 17; 75pp; English.
PS
XX The sequences represented by AAT00405-T00418 are genetic suppressor
CC elements (GSEs). This sequence represents GSE HL6.10. This sequence shows
CC homology to the cDNA encoding testosterone-repressed prostatic message-2
CC (TRPM-2). These sequences were obtained from a cDNA library derived from
CC the total cDNA of a cisplatin sensitive cell. Genetic suppressor elements
CC confer resistance to platinum-based drugs (pDs), such as cisplatin. These
CC functional GSEs can then be used to create probes for the parent gene.
CC The probes can then be used in a method of measuring the level of GSE
CC gene expression. The GSEs can be used in methods of diagnosis of
CC resistance to pDs by measuring the level of expression of GSE genes. The
CC GSEs are also used in methods to overcome resistance to pDs in cancer
CC cells. The GSEs (or fragments of them) can be used to inhibit the
CC function of genes associated with sensitivity to pDs. For enhancement of
CC chemotherapy, a GSE can be transferred (either alone or with another
CC gene) on an expression vector into blood progenitor cells from a cancer
CC patient. The cells are returned to the patients circulation and allowed
CC to repopulate the blood before aggressive chemotherapy is carried out
CC (using higher cisplatin concentrations than normal), this will thereby
CC avoid toxic side effects to the immune system as the blood cells will be
CC GSE resistant
XX
SQ Sequence 195 BP; 46 A; 45 C; 71 G; 33 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 195;

Best Local Similarity 100.0%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
|||||
Db 87 CAGCAGCAGAGTCTTCATCAT 67

RESULT 7
AAC06940/c
ID AAC06940 standard; cDNA; 275 BP.
XX
AC AAC06940;
XX
Dt 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 11015.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
DR
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 11015; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
SQ Sequence 275 BP; 59 A; 88 C; 85 G; 43 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 3; Length 275;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
|||||
Db 128 CAGCAGCAGAGTCTTCATCAT 108

RESULT 8
AAF94824/c
ID AAF94824 standard; cDNA; 396 BP.
XX

AC AAF94824;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human ovarian cancer associated coding sequence SEQ ID NO: 15.
XX
KW Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.
XX
OS Homo sapiens.
XX
PN WO200118046-A2.
XX
PD 15-MAR-2001.
XX
PF 08-SEP-2000; 2000WO-US024827.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Stolk JA;
XX
DR WPI; 2001-211395/21.
XX
PT Isolated polypeptides associated with ovarian carcinomas, and the nucleic
PT acids that encode them, useful for the prevention diagnosis and treatment
PT of ovarian cancers.
XX
PS Claim 18; Page 120; 189pp; English.
XX
CC The present invention provides a number of coding sequences and proteins,
CC the over-expression of which is associated with ovarian carcinoma/cancer.
CC These can be used in the diagnosis, treatment and prevention of ovarian
CC cancer, optionally by gene therapy or in the form of a vaccine. The
CC present sequence is an example of one of these sequences
XX
SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 0 U; 1 Other;

Query Match 100.0%; Score 21; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db |||||
79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 9
ABL48774/c
ID ABL48774 standard; cDNA; 396 BP.
XX
AC ABL48774;
XX
DT 18-JUN-2002 (first entry)
XX
DE Ovarian carcinoma sequence isolate 23657.1.
XX
KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
KW ss.
XX
OS Homo sapiens.
XX
PN US2002004491-A1.
XX
PD 10-JAN-2002.
XX
PF 03-APR-2001; 2001US-00825294.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.

PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
XX
PA (XUJJ/) XU J.
PA (STOL/) STOLK J A.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP;
XX
DR WPI; 2002-171027/22.
XX
PT Ovarian tumor polypeptide and polynucleotide useful in diagnosis,
PT prevention and/or treatment of cancer, especially ovarian cancer.
XX
PS Example 1; Page 43; 131pp; English.
XX
CC The invention relates to ovarian tumour polynucleotides and polypeptides
CC that may be utilised in cancer therapy, for example in a vaccine or gene
CC therapy. Polypeptides and polynucleotides of the invention are useful for
CC detecting a cancer in a patient, for stimulating and/or expanding T-cells
CC specific for a tumour protein, and for inhibiting the development of a
CC cancer in a patient. They are also useful for stimulating an immune
CC response in a patient, and for treating a cancer in a patient and for
CC determining the presence of a cancer in a patient. The isolated
CC polynucleotides of the invention are useful for their ability to
CC selectively form duplex molecules with complementary stretches of the
CC entire desired gene or gene fragments, and for designing and preparing
CC ribozyme molecules for inhibiting expression of tumour polypeptides in
CC tumour cells. Polypeptides and polynucleotides of the invention are also
CC useful in recombinant DNA molecules to direct expression of a polypeptide
CC in appropriate host cells. The sequences given in records ABL48760-
CC ABL48956 represent polynucleotides encoding ovarian carcinoma proteins
XX
SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 0 U; 1 Other;

Query Match 100.0%; Score 21; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db |||||
79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 10
ABT03091/c
ID ABT03091 standard; cDNA; 396 BP.
XX
AC ABT03091;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 15.
XX
KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
KW cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200239885-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US045395.
XX
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
XX
PA (CORI-) CORIXA CORP.
XX

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX WPI; 2002-500186/53.
XX Novel ovarian cancer polypeptide and polynucleotide, useful for detecting
PT the presence of ovarian cancer in a patient, and in pharmaceutical
PT compositions, e.g. vaccines, for treating ovarian cancer.
XX
PS Example 1; Page 117; 197pp; English.
XX
CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention
XX
SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 0 U; 1 Other;

Query Match 100.0%; Score 21; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 11
ADM10684/c
ID ADM10684 standard; cDNA; 396 BP.
XX
AC ADM10684;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian carcinoma-associated cDNA 23657.1.
XX
KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
KW cytostatic; gene therapy; human; ss.
XX
OS Homo sapiens.
XX
PN US2003206918-A1.
XX
PD 06-NOV-2003.
XX
PF 05-FEB-2003; 2003US-00361811.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Fling SP;
XX
DR WPI; 2003-901037/82.
XX
PT New polynucleotides encoding tumor proteins, treating or inhibiting the
PT development of cancer, particularly ovarian cancer, and for stimulating
PT and/or expanding T cells specific for a tumor protein.
XX
PS Example 1; SEQ ID NO 15; 221pp; English.
XX
CC This invention describes a novel ovarian tumour protein which can be used
CC to detecting the presence of an ovarian cancer in a patient by
CC stimulating and/or expanding T cells specific for the tumour protein. The
CC products of the invention can also be used in a method to inhibit the
CC development of a cancer in a patient comprising (a) incubating CD4+

CC and/or CD8+ T cells isolated from a patient with at least one ovarian
CC tumour protein, such that T cell proliferate and (b) administering to the
CC patient the proliferated T cells. The cytostatic polynucleotides or
CC polypeptides described in the invention are useful for treating or
CC inhibiting the development of cancer, particularly ovarian cancer and for
CC stimulating and/or expanding T cells specific for a tumour protein or for
CC gene therapy.
XX
SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 0 U; 1 Other;

Query Match 100.0%; Score 21; DB 11; Length 396;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 12
ADJ11014/c
ID ADJ11014 standard; cDNA; 396 BP.
XX
AC ADJ11014;
XX
DT 15-APR-2004 (first entry)
XX
DE Representative human ovarian carcinoma cDNA SeqID 15.
XX
KW human; ss; ovarian cancer; immunogenic; antibody;
KW antigen presenting cell; APC; immune system cell; T cell; tumourigenic;
KW cytostatic.
XX
OS Homo sapiens.
XX
PN US2003232056-A1.
XX
PD 18-DEC-2003.
XX
PF 14-FEB-2003; 2003US-00369186.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
PR 05-FEB-2003; 2003US-00361811.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Fling SP;
XX
DR WPI; 2004-178717/17.
XX
PT Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
PT polypeptide, useful as probes of primers for detecting presence of cancer
PT in a patient.
XX
PS Example 1; SEQ ID NO 15; 222pp; English.
XX
CC This invention relates to novel isolated polynucleotides and methods for
CC the therapy and diagnosis of cancer, particularly ovarian cancer.
CC Specifically, it refers to these polynucleotides and the encoded
CC polypeptides thereof, as well as immunogenic peptides, antibodies,
CC antigen presenting cells (APCs) and immune system cells (e.g. T cells)
CC that are targeted to those cells expressing the proteins of interest. The
CC present invention describes methods that are useful for stimulating and/
CC or expanding T cells specific for a tumourigenic protein (i.e. T cell
CC therapy). Furthermore, compositions can be used for the diagnosis,
CC treatment and/ or prevention of ovarian cancer by stimulating an immune

CC response in a patient. Accordingly, these compositions exhibit cytostatic
CC activity. This polynucleotide sequence is a representative human ovarian
CC carcinoma cDNA sequence of the invention.

XX
SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 0 U; 1 Other;
Query Match 100.0%; Score 21; DB 12; Length 396;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 13
ADM43275/c
ID ADM43275 standard; cDNA; 396 BP.

XX AC ADM43275;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human ovarian carcinoma cDNA #15.
XX
KW ss; human; cancer; ovarian cancer; ovarian carcinoma.
XX
OS Homo sapiens.
XX
PN US2003129192-A1.
XX
PD 10-JUL-2003.
XX
PF 02-AUG-2002; 2002US-00212677.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
XX
PA (CORI-) CORIXA CORP.
XX
PI Chenault RA, Xu J, Fanger GR, Harlocker SL, Mcneill PD;
XX
DR WPI; 2004-051070/05.
XX
PT New isolated polynucleotide encoding an ovarian tumor protein for use in
PT diagnosing, preventing or treating cancer, particularly ovarian cancer.
XX
PS Example 1; SEQ ID NO 15; 220pp; English.

XX
CC The invention relates to an isolated polynucleotide. The invention is
CC used to diagnose, prevent or treat cancer, particularly ovarian cancer.
CC The present sequence represents a human ovarian carcinoma cDNA.
XX
SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 0 U; 1 Other;
Query Match 100.0%; Score 21; DB 12; Length 396;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 14
ACH44960/c
ID ACH44960 standard; cDNA; 461 BP.
XX

AC ACH44960;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human foetal brain cDNA #5685.

XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX

PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Claim 1; SEQ ID NO 32172; 44pp; English.

XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ Sequence 461 BP; 139 A; 98 C; 144 G; 71 T; 0 U; 9 Other;
Query Match 100.0%; Score 21; DB 9; Length 461;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 130 CAGCAGCAGAGTCTTCATCAT 110

RESULT 15
ACH15312/c
ID ACH15312 standard; cDNA; 462 BP.
XX
AC ACH15312;
XX
DT 13-OCT-2003 (first entry)
XX

Human adult brain cDNA #2524.

Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
genome mapping; biodiversity; genetic disorder.

Homo sapiens.

US2003073623-A1.
17-APR-2003.
30-JUL-2001; 2001US-00918995.
30-JUL-2001; 2001US-00918995.
(DRMA/) DRMANAC R T.
(LABA/) LABAT I.
(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M C.
(JONE/) JONES L W.
Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
WPI; 2003-615964/58.

New polynucleotide sequences obtained from various cDNA libraries, useful
as hybridization probes, as oligomers for PCR, for chromosome and gene
mapping, in the recombinant production of protein, or in generating
antisense DNA or RNA.

Claim 1; SEQ ID NO 2524; 44pp; English.

The invention relates to an isolated polynucleotide comprising any one of
38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
determined by the technique of SBH (sequencing by hybridisation). Also
included is a purified polypeptide comprising a sequence corresponding to
a reading frame of the novel polynucleotide. The nucleic acid sequences
are useful in diagnostics as expressed sequence tags (EST) for
identifying expressed genes or for physical mapping of the human genome,
in forensics, in assessing biodiversities, or in identifying mutations
responsible for genetic disorders and other traits. The nucleotide
sequences are also useful as hybridisation probes, as oligomers for PCR,
for chromosome and gene mapping, in the recombinant production of
protein, or in generating antisense DNA or RNA. The purified polypeptide
is useful for generating antibodies specific for it. The present sequence
is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
for this patent did not form part of the printed specification, but was
obtained in electronic format directly from USPTO at
seqdata.uspto.gov/sequence.html?DocID=20030073623

Sequence 462 BP; 146 A; 100 C; 142 G; 72 T; 0 U; 2 Other;

Query Match 100.0%; Score 21; DB 9; Length 462;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 CAGCAGCAGAGTCTTCATCAT 21
| | | | | | | | | | | |
Db 115 CAGCAGCAGAGTCTTCATCAT 95

Search completed: March 22, 2005, 10:05:03
Job time : 238 secs

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 09:42:30 ; Search time 88 Seconds
(without alignments)
390.475 Million cell updates/sec

Title: US-10-646-391A-4
Perfect score: 21
Sequence: 1 cagcagcagagtcttcatcat 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	100.0	181	2	US-08-485-657A-19
C 2	21	100.0	181	4	US-09-366-380-19
C 3	21	100.0	181	5	PCT-US95-02303-18
C 4	21	100.0	195	2	US-08-485-657A-14
C 5	21	100.0	195	4	US-09-366-380-14
C 6	21	100.0	195	5	PCT-US95-02303-14
C 7	21	100.0	275	4	US-09-513-999C-11015
C 8	21	100.0	396	4	US-09-640-173-15
C 9	21	100.0	396	4	US-09-713-550-15
C 10	21	100.0	396	4	US-09-825-294-15
C 11	21	100.0	396	4	US-09-970-966-15
C 12	21	100.0	482	4	US-09-621-976-13267
C 13	21	100.0	491	4	US-09-513-999C-3749
C 14	21	100.0	601	4	US-09-949-016-201815
C 15	21	100.0	1648	3	US-09-659-791A-3
C 16	21	100.0	1651	3	US-09-659-791A-13
C 17	21	100.0	1825	4	US-09-949-016-5661
C 18	21	100.0	7610	3	US-09-659-791A-12
C 19	21	100.0	17348	4	US-09-949-016-17403
C 20	17.8	84.8	50	4	US-09-485-632B-15
C 21	17.8	84.8	448	4	US-09-513-999C-14310
C 22	17.8	84.8	601	4	US-09-949-016-139518
C 23	17.8	84.8	117001	4	US-09-949-016-15684
C 24	17.4	82.9	492	4	US-09-621-976-3772
C 25	17.4	82.9	633	3	US-08-950-925-1
C 26	17.4	82.9	633	4	US-09-565-286-1
C 27	17.4	82.9	651	2	US-08-961-858-1

C 28	17.4	82.9	651	2	US-08-961-858-3	Sequence 3, Appli
C 29	17.4	82.9	651	3	US-09-089-593-1	Sequence 1, Appli
C 30	17.4	82.9	651	3	US-09-089-593-3	Sequence 3, Appli
C 31	17.4	82.9	651	3	US-08-993-380-5	Sequence 5, Appli
C 32	17.4	82.9	744	4	US-09-368-819A-1	Sequence 1, Appli
C 33	17.4	82.9	785	4	US-09-949-016-2557	Sequence 2557, Ap
C 34	17.4	82.9	795	4	US-09-368-819A-3	Sequence 3, Appli
C 35	17.4	82.9	1173	3	US-08-993-380-3	Sequence 3, Appli
C 36	17.2	81.9	181	4	US-09-513-999C-26550	Sequence 26550, A
C 37	16.8	80.0	198	4	US-09-248-796A-8114	Sequence 8114, Ap
C 38	16.8	80.0	234	4	US-09-248-796A-11572	Sequence 11572, A
C 39	16.8	80.0	330	2	US-08-980-060-9	Sequence 9, Appli
C 40	16.8	80.0	330	3	US-09-307-185-9	Sequence 9, Appli
C 41	16.8	80.0	330	4	US-09-773-753-9	Sequence 9, Appli
C 42	16.8	80.0	334	3	US-09-227-357-90	Sequence 90, Appl
C 43	16.8	80.0	601	4	US-09-949-016-173228	Sequence 173228,
C 44	16.8	80.0	601	4	US-09-949-016-173229	Sequence 173229,
C 45	16.8	80.0	1806	2	US-08-980-060-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-485-657A-19/c
; Sequence 19, Application US/08485657A
; Patent No. 5942389
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,657A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5942389nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-485-657A-19

Query Match 100.0%; Score 21; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CAGCAGCAGAGTCTTCATCAT 21
|||||||

Db 73 CAGCAGCAGAGTCTTCATCAT 53

RESULT 2

US-09-366-380-19/c
; Sequence 19, Application US/09366380
; Patent No. 6541603
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366.380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,900
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6541603nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-366-380-19

Query Match 100.0%; Score 21; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21

Db 73 CAGCAGCAGAGTCTTCATCAT 53

RESULT 3

PCT-US95-02303-18/c
; Sequence 18, Application PC/TUS9502303
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:

Query Match 100.0%; Score 21; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21

Db 73 CAGCAGCAGAGTCTTCATCAT 53

APPLICATION NUMBER: PCT/US95/02303
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US95-02303-18

Query Match 100.0%; Score 21; DB 5; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21

Db 73 CAGCAGCAGAGTCTTCATCAT 53

RESULT 4

US-08-485-657A-14/c
; Sequence 14, Application US/08485657A
; Patent No. 5942389
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,657A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5942389nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-485-657A-14

Query Match 100.0%; Score 21; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21

Db 87 CAGCAGCAGAGTCTTCATCAT 67

RESULT 5

US-09-366-380-14/c
; Sequence 14, Application US/09366380
; Patent No. 6541603
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,900
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6541603nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-366-380-14

Query Match 100.0%; Score 21; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 87 CAGCAGCAGAGTCTTCATCAT 67

RESULT 6
PCT-US95-02303-14/c
; Sequence 14, Application PC/TUS9502303
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02303
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US95-02303-14

Query Match 100.0%; Score 21; DB 5; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 87 CAGCAGCAGAGTCTTCATCAT 67

RESULT 7
US-09-513-999C-11015/c
; Sequence 11015, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 11015
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-11015

Query Match 100.0%; Score 21; DB 4; Length 275;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 128 CAGCAGCAGAGTCTTCATCAT 108

RESULT 8
US-09-640-173-15/c
; Sequence 15, Application US/09640173
; Patent No. 6613515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 210121.484C2
; CURRENT APPLICATION NUMBER: US/09/640,173
; CURRENT FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-173-15

Query Match 100.0%; Score 21; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.1;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTTCATCAT 21
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Db 79 CAGCAGCAGAGTCTTTCATCAT 59

RESULT 9
US-09-713-550-15/c
; Sequence 15, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; * TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-15

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Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTTCATCAT 21
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Db 79 CAGCAGCAGAGTCTTTCATCAT 59

RESULT 10
US-09-825-294-15/c
; Sequence 15, Application US/09825294
; Patent No. 6710170
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; * APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-15

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTTCATCAT 21
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Db 79 CAGCAGCAGAGTCTTTCATCAT 59

RESULT 11
US-09-970-966-15/c
; Sequence 15, Application US/09970966
; Patent No. 6720146
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Molesch, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 333
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-15

Query Match 100.0%; Score 21; DB 4; Length 396;
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTTCATCAT 21
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Db 79 CAGCAGCAGAGTCTTTCATCAT 59

RESULT 12
US-09-621-976-13267/c
; Sequence 13267, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13267
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13267

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Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTTCATCAT 21
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Db 96 CAGCAGCAGAGTCTTTCATCAT 76

RESULT 13
US-09-513-999C-3749/c
; Sequence 3749, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 3749
LENGTH: 491
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 108..455
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 108..161
OTHER INFORMATION: score 6.3
OTHER INFORMATION: seq LLFVGLLLTWESG/QV
FEATURE:
NAME/KEY: misc_feature
LOCATION: 459
OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-3749

Query Match 100.0%; Score 21; DB 4; Length 491;
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QY 1 CAGCAGCAGAGTCTTCATCAT 21
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Db 128 CAGCAGCAGAGTCTTCATCAT 108

RESULT 14
US-09-949-016-201815
Sequence 201815, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 201815
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-201815

Query Match 100.0%; Score 21; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
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Db 548 CAGCAGCAGAGTCTTCATCAT 568

RESULT 15
US-09-659-791A-3/c

Sequence 3, Application US/09659791A
Patent No. 6383808
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
FILE REFERENCE: RTS-0156
CURRENT APPLICATION NUMBER: US/09/659,791A
CURRENT FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 3
LENGTH: 1648
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (53)...(1402)
US-09-659-791A-3

Query Match 100.0%; Score 21; DB 3; Length 1648;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
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Db 73 CAGCAGCAGAGTCTTCATCAT 53

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Job time : 89 secs

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 10:02:41 ; Search time 281 Seconds
(without alignments)
444.903 Million cell updates/sec

Title: US-10-646-391A-4
Perfect score: 21
Sequence: 1 cagcagcagagtcttcattcat 21

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Searched: 5544816 seqs, 2976611598 residues

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Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	21	100.0	21	9	US-09-944-326-4
2	21	100.0	21	10	US-09-967-726A-4
3	21	100.0	21	16	US-10-080-794-4
4	21	100.0	21	17	US-10-646-391A-4
5	21	100.0	21	18	US-10-828-394-5
6	21	100.0	21	18	US-10-828-395-5
7	21	100.0	23	17	US-10-646-436-66
8	21	100.0	181	17	US-10-404-579-19
9	21	100.0	195	17	US-10-404-579-14
10	21	100.0	255	17	US-10-242-535A-37963
11	21	100.0	255	17	US-10-085-783A-37963
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					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 5, Appli
					Sequence 5, Appli
					Sequence 66, Appl
					Sequence 19, Appl
					Sequence 14, Appl
					Sequence 37963, A
					Sequence 37963, A

C 12	21	100.0	270	17	US-10-242-535A-33018	Sequence 33018, A
C 13	21	100.0	270	17	US-10-085-783A-33018	Sequence 33018, A
C 14	21	100.0	306	17	US-10-242-535A-28941	Sequence 28941, A
C 15	21	100.0	306	17	US-10-085-783A-28941	Sequence 28941, A
C 16	21	100.0	346	19	US-10-696-639-2963	Sequence 2963, Ap
C 17	21	100.0	396	9	US-09-825-294-15	Sequence 15, Appl
C 18	21	100.0	396	9	US-09-970-966-15	Sequence 15, Appl
C 19	21	100.0	396	15	US-10-212-677-15	Sequence 15, Appl
C 20	21	100.0	396	17	US-10-361-811-15	Sequence 15, Appl
C 21	21	100.0	396	17	US-10-369-186-15	Sequence 15, Appl
C 22	21	100.0	461	10	US-09-918-995-32172	Sequence 32172, A
C 23	21	100.0	462	10	US-09-918-995-2524	Sequence 2524, Ap
C 24	21	100.0	465	10	US-09-918-995-32177	Sequence 32177, A
C 25	21	100.0	490	10	US-09-918-995-12511	Sequence 12511, A
C 26	21	100.0	491	10	US-09-918-995-17455	Sequence 17455, A
C 27	21	100.0	492	10	US-09-918-995-31156	Sequence 31156, A
C 28	21	100.0	704	17	US-10-264-049-1985	Sequence 1985, Ap
C 29	21	100.0	1067	19	US-10-491-213-91	Sequence 91, Appl
C 30	21	100.0	1117	19	US-10-491-213-93	Sequence 93, Appl
C 31	21	100.0	1315	19	US-10-491-213-101	Sequence 101, App
C 32	21	100.0	1369	19	US-10-491-213-90	Sequence 90, Appl
C 33	21	100.0	1373	19	US-10-491-213-102	Sequence 102, App
C 34	21	100.0	1451	16	US-10-133-013-214	Sequence 214, App
C 35	21	100.0	1568	17	US-10-291-172-29	Sequence 29, Appl
C 36	21	100.0	1568	17	US-10-221-278-29	Sequence 29, Appl
C 37	21	100.0	1610	19	US-10-491-213-89	Sequence 89, Appl
C 38	21	100.0	1614	16	US-10-119-428-31	Sequence 31, Appl
C 39	21	100.0	1648	17	US-10-380-124-3	Sequence 3, Appli
C 40	21	100.0	1651	17	US-10-380-124-13	Sequence 13, Appl
C 41	21	100.0	1651	18	US-10-717-597-63	Sequence 63, Appl
C 42	21	100.0	1651	19	US-10-278-698-139	Sequence 139, App
C 43	21	100.0	1651	19	US-10-278-698-655	Sequence 655, App
C 44	21	100.0	1676	17	US-10-646-391A-1	Sequence 1, Appli
C 45	21	100.0	1676	18	US-10-283-975A-259	Sequence 259, App

ALIGNMENTS

RESULT 1
US-09-944-326-4
; Sequence 4, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-4

Query Match 100.0%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred.No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGTCTTCATCAT 21
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Db 1 CAGCAGCAGAGTCTTCATCAT 21

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RESULT 2
US-09-967-726A-4
; Sequence 4, Application US/09967726A
; Publication No. US20030158130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: UBC.P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-09-967-726A-4

Query Match      100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 3
US-10-080-794-4
; Sequence 4, Application US/10080794
; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; TITLE OF INVENTION: HAVING 2'-O-(2-METHOXY)ETHYL MODIFICATIONS
; FILE REFERENCE: UBC.P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-4

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Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 4
US-10-646-391A-4
; Sequence 4, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
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; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-646-391A-4

Query Match      100.0%; Score 21; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 5
US-10-828-394-5
; Sequence 5, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; FILE REFERENCE: UBC.P-033
; CURRENT APPLICATION NUMBER: US/10/828,394
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-394-5

Query Match      100.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 6
US-10-828-395-5
; Sequence 5, Application US/10828395
; Publication No. US20040224914A1
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; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders
; FILE REFERENCE: UBC.P-032
; CURRENT APPLICATION NUMBER: US/10/828,395
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/464,160
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-395-5

Query Match      100.0%; Score 21; DB 18; Length 21;
* Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCAGCAGAGTCTTCATCAT 21
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Db      1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 7
US-10-646-436-66/c
; Sequence 66, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; APPLICANT: Signaevsky, Maxim
; APPLICANT: Beraldi, Eliana
; APPLICANT: Trougakos, Ioannis
; APPLICANT: Gonos, Efsthathios
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
; FILE REFERENCE: UBC.P-030
; CURRENT APPLICATION NUMBER: US/10/646,436
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 23
; TYPE: DNA
; ORGANISM: human
US-10-646-436-66

Query Match      100.0%; Score 21; DB 17; Length 23;
* Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCAGCAGAGTCTTCATCAT 21
      |||||
Db      23 CAGCAGCAGAGTCTTCATCAT 3

RESULT 8
US-10-404-579-19/c
; Sequence 19, Application US/10404579
; Publication No. US20040002099A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Kirschling, Deborah J
; Gudkov, Andrei
; Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/404,579
; FILING DATE: 01-Apr-2003
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,657A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20040002099A1nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-404-579-19

Query Match      100.0%; Score 21; DB 17; Length 181;
* Best Local Similarity 100.0%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCAGCAGAGTCTTCATCAT 21
      |||||
Db      73 CAGCAGCAGAGTCTTCATCAT 53

RESULT 9
US-10-404-579-14/c
; Sequence 14, Application US/10404579
; Publication No. US20040002099A1
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J
; Gudkov, Andrei
; Roninson, Igor B
; TITLE OF INVENTION: Genes and Genetic Elements Associated
; with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/404,579
FILING DATE: 01-Apr-2003
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/485,657A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. US20040002099Alnan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-10-404-579-14

Query Match 100.0%; Score 21; DB 17; Length 195;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
Db 87 CAGCAGCAGAGTCTTCATCAT 67

RESULT 10

US-10-242-535A-37963/c
Sequence 37963, Application US/10242535A
Publication No. US20040013663A1

GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 37963
LENGTH: 255
TYPE: DNA
ORGANISM: Human

US-10-242-535A-37963

Query Match 100.0%; Score 21; DB 17; Length 255;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
Db 97 CAGCAGCAGAGTCTTCATCAT 77

RESULT 11

US-10-085-783A-37963/c
Sequence 37963, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 37963
LENGTH: 255
TYPE: DNA
ORGANISM: Human
US-10-085-783A-37963

Query Match 100.0%; Score 21; DB 17; Length 255;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
Db 97 CAGCAGCAGAGTCTTCATCAT 77

RESULT 12

US-10-242-535A-33018/c
Sequence 33018, Application US/10242535A
Publication No. US20040013663A1

GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 33018
LENGTH: 270
TYPE: DNA
ORGANISM: Human
US-10-242-535A-33018

Query Match 100.0%; Score 21; DB 17; Length 270;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
Db 62 CAGCAGCAGAGTCTTCATCAT 42

RESULT 13

US-10-085-783A-33018/c
Sequence 33018, Application US/10085783A
Publication No. US20040037841A1

```

; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33018
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-33018

Query Match      100.0%; Score 21; DB 17; Length 270;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCAGCAGAGTCTTCATCAT 21
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Db      62 CAGCAGCAGAGTCTTCATCAT 42

RESULT 14
US-10-242-535A-28941/c
; Sequence 28941, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28941
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-28941

Query Match      100.0%; Score 21; DB 17; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCAGCAGAGTCTTCATCAT 21
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Db      98 CAGCAGCAGAGTCTTCATCAT 78

RESULT 15
US-10-085-783A-28941/c
; Sequence 28941, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
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; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28941
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-28941

Query Match      100.0%; Score 21; DB 17; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CAGCAGCAGAGTCTTCATCAT 21
      |||||||||||||||||||||
Db      98 CAGCAGCAGAGTCTTCATCAT 78

Search completed: March 22, 2005, 11:04:23
Job time : 281 secs
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This page Blank (uspto)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 09:35:40 ; Search time 1737 Seconds
(without alignments)
460.190 Million cell updates/sec

Title: US-10-646-391A-4
Perfect score: 21
Sequence: 1 cagcagcagagtcttcatcat 21
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
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5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	85	2	AW276802 xp66a01.x
2	21	100.0	100	2	BF920141 MR1-NT017
3	21	100.0	102	4	BF958934 PM1-NN120
4	21	100.0	119	2	AW901233 CM4-NN101
5	21	100.0	124	4	BM821731 K-EST0090
6	21	100.0	136	6	CD612966 56043322J
7	21	100.0	137	6	CD612965 56043322H
8	21	100.0	138	5	BQ339862 PM1-NN120
9	21	100.0	142	7	D45267 HUMHG1194 H
10	21	100.0	147	5	BQ339466 PM1-NN120
11	21	100.0	148	2	BF846357 PM1-EN006
12	21	100.0	149	7	R47195 CBS-389 Sub
13	21	100.0	169	2	BE766895 RC2-NT011
14	21	100.0	177	1	AL048592 DKFZp586H
15	21	100.0	183	4	BI032792 MR4-NN018
16	21	100.0	184	4	BF958930 PM1-NN120
17	21	100.0	185	4	BI036860 MR4-NT014
18	21	100.0	196	1	AI745406 wc37d01.x
19	21	100.0	197	4	BI036862 MR4-NT014
20	21	100.0	201	4	BF957666 PM1-NN120
21	21	100.0	203	4	BF957653 PM1-NN120
22	21	100.0	207	4	BF957858 PM1-NN120
23	21	100.0	224	2	AW161224 au70a10.Y
24	21	100.0	226	2	BF935119 MR4-NT014

25	21	100.0	236	4	BF948789 MR3-NN021
26	21	100.0	238	2	BF923639 MR4-NT014
27	21	100.0	239	4	BG898974 HOA21-1-C
28	21	100.0	241	7	CR767137 DKFZp469B
29	21	100.0	243	1	AA336628 EST41242
30	21	100.0	244	2	BE766870 RC2-NT011
31	21	100.0	248	2	BF923643 MR4-NT014
32	21	100.0	249	4	BF945175 PM1-NN120
33	21	100.0	250	5	BQ345410 MR4-NT014
34	21	100.0	252	2	BF923633 MR4-NT014
35	21	100.0	252	4	BF963107 PM1-NN120
36	21	100.0	253	2	BF887875 QV2-TN017
37	21	100.0	253	4	BI041998 MR4-NT014
38	21	100.0	256	4	BI041248 MR4-NT014
39	21	100.0	257	6	CD612964 56037472J
40	21	100.0	258	4	BF961150 PM1-NN120
41	21	100.0	258	7	CR763018 DKFZp469G
42	21	100.0	262	4	BF947155 MR3-NN021
43	21	100.0	262	5	BQ339859 PM1-NN120
44	21	100.0	263	2	BE899032 601682590
45	21	100.0	265	4	BF961152 PM1-NN120

ALIGNMENTS

RESULT 1
AW276802/c
LOCUS AW276802 85 bp mRNA linear EST 03-JAN-2000
DEFINITION xp66a01.x1 NCI CGAP Ov39 Homo sapiens cDNA clone IMAGE:2745288 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AW276802
VERSION AW276802.1 GI:6663832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 85)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Andrew Berchuck M.D., John Gillespie M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco.

FEATURES
Location/Qualifiers
1..85
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2745288"
/sex="female"
/tissue_type="papillary serous ovarian metastasis"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ov39"
/note="Organ: ovary; Vector: pAMP10; cDNA made by oligo-dt priming. Non-directionally cloned into the UDG sites of pAMP10. Size-selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. cDNA Library Preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 119)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL
MEDLINE

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED

20202663

COMMENT

10737800

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=CM4-NN1011-100

300-110-g04&t3=2000-03-10&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 11

High quality sequence stop: 118.

FEATURES

source

1. .119

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="NN1011"

/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 69;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 CAGCAGCAGAGTCTTCATCAT 21

Db

103 CAGCAGCAGAGTCTTCATCAT 83

RESULT 5

BM821731/c

LOCUS

BM821731 124 bp mRNA linear EST 06-MAR-2002

DEFINITION

K-EST0090952 S20T665307 Homo sapiens cDNA clone S20T665307-15-H01

5', mRNA sequence.

ACCESSION

BM821731

VERSION

BM821731.1 GI:19178144

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 124)

AUTHORS

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

21C Frontier Korean EST Project 2001

JOURNAL

Unpublished (2002)

COMMENT

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 15 row: H column: 01

High quality sequence stop: 124.

FEATURES

Location/Qualifiers

source

1. .124

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S20T665307-15-H01"

/sex="M"

/lab_host="Top10F"

/clone_lib="S20T665307"

/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was

adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transfection of competent cells E. coli Top10F' by electroporation method.

The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 21; DB 4; Length 124;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 CAGCAGCAGAGTCTTCATCAT 21

Db

102 CAGCAGCAGAGTCTTCATCAT 82

RESULT 6

CD612966

LOCUS

CD612966 136 bp mRNA linear EST 12-JAN-2004

DEFINITION 56043322J1 FLP Homo sapiens cDNA, mRNA sequence.

ACCESSION

CD612966

VERSION

CD612966.1 GI:40261230

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 136)

REFERENCE

AUTHORS

Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.

TITLE

Circular rapid amplification of cDNA ends for high-throughput

extension cloning of partial genes

JOURNAL

Genomics 84 (1), 205-210 (2004)

COMMENT

Contact: Fu GK

Incyte Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

Tel: 6508454102

Email: gfu@incyte.com.

FEATURES

source

1. .136

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="FLP"

/note="Vector: pDrive Cloning Vector"

ORIGIN

Best Local Similarity 100.0%; Pred. No. 71; Mismatches 0; Indels 0; Gaps 0; Matches 21; Conservative 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
| | | | | | | | | | | | | | | | | | | | |
Db 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 10
BQ339466

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BQ339466
PM1-NN1200-051100-004-h12 NN1200 Homo sapiens cDNA, mRNA sequence.
BQ339466
BQ339466.1 GI:20999152
EST.
Homo sapiens (human)

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 147)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
MEDLINE
PUBMED

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM1&t2=PM1-NN1200-051100-004-h12&t3=2000-11-05&t4=1)

Seq primer: puc 18 forward
High quality sequence stop: 34.

FEATURES
source
Location/Qualifiers
1..147
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1200"
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 21; DB 5; Length 147;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
| | | | | | | | | | | | | | | | | | | | |
Db 122 CAGCAGCAGAGTCTTCATCAT 142

RESULT 11
BF846357

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF846357
PM1-EN0065-231000-002-b01 EN0065 Homo sapiens cDNA, mRNA sequence.
BF846357
BF846357.1 GI:12233611
EST.
Homo sapiens (human)

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 148)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
MEDLINE
PUBMED

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM1&t2=PM1-EN0065-231000-002-b01&t3=2000-10-23&t4=1)

Seq primer: puc 18 forward
High quality sequence stop: 110.

FEATURES
source
Location/Qualifiers
1..148
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="EN0065"
/note="Organ: lung normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
| | | | | | | | | | | | | | | | | | | | |
Db 34 CAGCAGCAGAGTCTTCATCAT 54

RESULT 12
R47195/c

LOCUS
DEFINITION

R47195
CBS-389 Subtractive cDNA library ocular ciliary body Homo sapiens cDNA clone CBS-389 5' end similar to TRPM-2 (clusterin) (accession number M64722), mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

R47195
R47195.1 GI:807537
EST.
Homo sapiens (human)

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 149)
AUTHORS Escribano,J., Ortego,J. and Coca-Prados,M.
TITLE Isolation and characterization of cell-specific cDNA clones from a subtractive library of the ocular ciliary body of a single normal human donor: Transcription and synthesis of plasma proteins
JOURNAL J. Biochem. 118 (5), 921-931 (1995)
MEDLINE 96318503
PUBMED 8749308
COMMENT Contact: Coca-Prados, M.
Department of Ophthalmology and Visual Science
Yale University Medical School
330 Cedar Street, New Haven, CT 06520-8061
Tel: 2037852742
Fax: 2037856123
Email: miguel.coca-prados@quickmail.yale.edu
Seq primer: T3.
Location/Qualifiers
1..149
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CBS-389"
/clone_lib="Subtractive cDNA library ocular ciliary body"
/note="Vector: pBluescript II SK; Site_1: EcoRI; Site_2: XhoI; A subtractive cDNA library was developed by hybridizing antisense, single-stranded phagemid DNA (ssDNA) (as pBluescript SK-) from the ocular ciliary body cDNA library (target) of a 34-year-old female donor in lambda-Uni-ZAP XR with biotinylated sense RNA of an ocular cell line cDNA library (driver) in the same vector."

ORIGIN
Query Match 100.0%; Score 21; DB 7; Length 149;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
|||||
Db 71 CAGCAGCAGAGTCTTCATCAT 51

RESULT 13
BE766895/c
LOCUS BE766895 169 bp mRNA linear EST 19-SEP-2000
DEFINITION RC2-NT0110-050600-013-f03 NT0110 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE766895
VERSION BE766895.1 GI:10196819
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 169)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC2-NT0110-050600-013-f03&t3=2000-06-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 169.
Location/Qualifiers
1..169
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0110"
/note="Organ: nervous tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES
source
ORIGIN
Query Match 100.0%; Score 21; DB 2; Length 169;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATCAT 21
|||||
Db 59 CAGCAGCAGAGTCTTCATCAT 39

RESULT 14
AL048592/c
LOCUS AL048592 177 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp586H092_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586H092, mRNA sequence.
ACCESSION AL048592
VERSION AL048592.1 GI:4729143
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177)
Poustka,A., Klein,M., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Poustka, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZp586H092) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..177
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp586H092"
/tissue_type="uterus"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="586 (synonym: hute1)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"

FEATURES
source
ORIGIN

Query Match 100.0%; Score 21; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 77 CAGCAGCAGAGTCTTCATCAT 57

RESULT 15
BI032792
LOCUS BI032792 183 bp mRNA linear EST 14-JUN-2001
DEFINITION MR4-NN0188-220101-204-e01 NN0188 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI032792
VERSION BI032792.1 GI:14439418
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 183)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-NN0188-
220101-204-e01&t3=2001-01-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 183.

FEATURES
Location/Qualifiers
1..183
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN0188"
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 100.0%; Score 21; DB 4; Length 183;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 69 CAGCAGCAGAGTCTTCATCAT 89

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